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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/081,775

DATE: 03/20/2002
TIME: 11:25:58

Input Set : A:\PTO.VSK.txt

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3 <110> APPLICANT: Bristol-Myers Squibb Company
      5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED
              RECEPTOR, HGPRBMY25, EXPRESSED HIGHLY IN IMMUNE-RELATED TISSUES
      8 <130> FILE REFERENCE: D0126 NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/081,775
C--> 10 <141> CURRENT FILING DATE: 2002-02-21
     10 <150> PRIOR APPLICATION NUMBER: US 60/270,134
     11 <151> PRIOR FILING DATE: 2001-02-21
     13 <150> PRIOR APPLICATION NUMBER: US 60/278,952
    14 <151> PRIOR FILING DATE: 2001-03-27
    16 <160> NUMBER OF SEQ ID NOS: 69
    18 <170> SOFTWARE: PatentIn version 3.0
    20 <210> SEQ ID NO: 1
    21 <211> LENGTH: 1567
    22 <212> TYPE: DNA
    23 <213> ORGANISM: homo sapiens
    25 <220> FEATURE:
    26 <221> NAME/KEY: CDS
    27 <222> LOCATION: (537)..(1523)
    29 <400> SEQUENCE: 1
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    32 gacaagaaaa aaaaagtcca agattaccca gtgaactatg tttgtagttt gtgtcaccaa
                                                                              120
    34 actgatagtc acgcctaatt tcttcttata ctccataaaa gacagtgtgt atgtatgtgt
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    36 gtgtgtttct ttgtgtgtat gtatgtattc aggtatatgt gtatagcctt agctaggaga
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    38 caattotagt ttatotaaag gottatttga goodttote acgttoattt attttattta
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    40 ataagcatta tatatcaggt attattcaaa gctctttaga aatctttaga catattaacc
                                                                             360
    42 catataattc tcttctctat agggaataga tatgattatt attgctattt tatggatgat
                                                                             420
    44 gaagetttet aaacatgtta tageeagtaa gtgttaetat teteteatte etatetetgt
                                                                             480
    46 totatottgt tootcoagat aatgtgatac tatgtggagg tttotgacca cagaga atg
                                                                             539
    47
                                                                      Met
    48
                                                                      1
    50 tee age act ett gge eac aac atg gaa tet eet eat eac act gat gtt
                                                                             587
    51 Ser Ser Thr Leu Gly His Asn Met Glu Ser Pro His His Thr Asp Val
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    54 gac cct tct gtc ttc ttc ctc ctg ggc atc cca ggt ctg gaa caa ttt
                                                                             635
    55 Asp Pro Ser Val Phe Phe Leu Leu Gly Ile Pro Gly Leu Glu Gln Phe
                                   25
    58 cat ttg tgg ctc tca ctc cct gtg tgt ggc tta ggc aca gcc aca att
                                                                             683
   59 His Leu Trp Leu Ser Leu Pro Val Cys Gly Leu Gly Thr Ala Thr Ile
   60
           35
   62 gtg ggc aat ata act att ctg gtt gtt gtt gcc act gaa cca gtc ttg
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   63 Val Gly Asn Ile Thr Ile Leu Val Val Val Ala Thr Glu Pro Val Leu
   64 50
                           55
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70) qct	. acc	tet	ato		' aca	att	000		75					80	tgt	
71 72		Ala	Ser	Val 85	Ser	Thr	· Val	Pro	Lys 90	Leu	Leu	gct Ala	atc Ile	Phe	tgg Trp	tgt Cys	827
74	gga	gcc	gga	cat	. ata	tet	acc	tct	acc	+ 400	a+ a			95		ttc	
75 76	011	Āla	Gly 100	1113	Ile	Ser	Ala	Ser	Ala	Cys	Leu	gca Ala	His	atg Met	ttc Phe	ttc Phe	875
78	att	cat	qcc	ttc	tgc	ato	ato	TOD	too	3.0±	~+~		110				
79 80		His 115	ALG	Phe	Cys	Met	мет	Glu	Ser	Thr	Val	Leu	ctg Leu	gcc Ala	atg Met	gcc Ala	923
0.0		110					120					1 2 5					
83	Dho	yat	2ge	tac	gtg	gcc	atc	tgc	cac	cca	ctc	cgc	tat	gcc	aca	atc	971
84	130	5p	nig	1 y 1	Val	135	116	Cys	His	Pro	Leu	Arg	Tyr	Ala	Thr	Ile	
86	ctc	act	gac	acc	atc	att	gcc	cac	ata	qqq	qtq	qca	act	αta	ata		1019
88			1.57	1111	150	TIE	Ald	HIS	rre	GLY 155	Val	Ala	Ala	Val	Val	Arg	1019
90	ggc	tcc	ctg	ctc	atg	ctc	сса	tat	CCC	tta	+++	a + +	~~~	~ ~ 4	160		
91	Gly	Ser	Leu	Leu	Met	Leu	Pro	Cvs	Pro	Pho	Dho	TIO	999 Cl.,	Cg L	LEG	aac	1067
				T 0 3					170					175			
94	ttc	tgc	caa	agc	cat	gtg	atc	cta	cac	acα	tac	tat	gag		2 t ~	~~+	1115
	Phe	Cys	Gln	Ser	His	Val	Ile	Leu	His	Thr	Tvr	Cvs	Glu	Hic	aly Mot	9CL	1115
			100					185					100				
98	gtg	gtg	aag	ctg	gcc	tgt	gga	gac	acc	agg	cct	aac		ata	tat	aaa	1163
		· uı	Lys	Leu	Ala	Cys	Gly	Asp	Thr	Arg	Pro	Asn	Arg	Val	Tvr	Glv	1103
		1)					2.00					205					
102	ctg	aca	gct	gca	ctg	ttg	gtc	att	ggg	gtt	gac	ttg	ttt	tqc	att	ggt	1211
	210	7 111	. Ala	Ala	Leu	Leu	vaı	Ile	Gly	Val	Asp	Leu	Phe	Cys	Ile	ggt Gly	1211
						210					าาก						
100	Lou	Con	Lat	gcc	cta	att	gca	caa	gct	gtc	ctt	cgc	ctc	tca	tcc	cat	1259
108	Lea	oci	1 1 1	АТа	230	тте	Ala	GIn	Ala	Val	Leu	Arg	Leu	Ser	Ser	His	_
110	gaa	gct	cgg	tcc	aag	gcc	cta	ggg	acc	tgt	ggt	tcc	cat	atc		atc	1307
	GIu	Ala	Arg	ser	Lys	Ala	Leu	Gly	Thr	Cys	Gly	Ser	His	Val	Cvs	Val	1307
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114	atc	Ctc	atc	tct	tat	aca	cca	gcc	ctc	ttc	tcc	ttt	ttt		cac	cac	1355
	11e	Leu	116	Ser	1 y I	THE	Pro	Ala	Leu	Phe	Ser	Phe	Phe	Thr	His	Ara	1333
			200					265					270				
110	Dha	ggc	cat	cac	gtt	cca	gtc	cat	att	cac	att	ctt	ttg	gcc	aat	att	1403
120	РПе	275	HIS	HIS	Val	Pro	val	His	Ile	His	Ile	Leu	Leu	Ala	Asn	Val	
		2/5					280					205					
123	Tur	tou	CLL	ttg	cca	cct	gct	ctt	aat	cct	gtg	gta	tat	gga	gtt	aaq	1451
124	- 1 -	Leu	Leu	Leu	Pro	PIO	Ala	Leu	Asn	Pro	Val	Val	Tyr	Gly	Val	Lys	· -
						290					300					~ ~ ~	
127	Thr	Luc	Cln	TIA	cgt	aaa	aga	gtt	gtc	agg	gtg	ttt	caa	agt	ggg	cag	1499
128	1111	Lys	GIII	тте	Arg 310	гàг	Arg	Val	Val	Arg	Val	Phe	Gln	Ser	Gly	Gln	
					2 TU					315					2 2 2		
	J 5 G	409	990	ull	aay	yca	LCT	gag	tgac	cctg	ga g	tata	gagg	g ac	ttaa	tcca	1553

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131 Gly Met Gly Ile Lys Ala Ser Glu 132 325 134 aaaaaaaaa aaaa 1567 137 <210> SEQ ID NO: 2 138 <211> LENGTH: 329 139 <212> TYPE: PRT 140 <213> ORGANISM: homo sapiens 142 <400> SEQUENCE: 2 144 Met Ser Ser Thr Leu Gly His Asn Met Glu Ser Pro His His Thr Asp 10 148 Val Asp Pro Ser Val Phe Phe Leu Leu Gly Ile Pro Gly Leu Glu Gln 20 2.5 152 Phe His Leu Trp Leu Ser Leu Pro Val Cys Gly Leu Gly Thr Ala Thr 40 156 Ile Val Gly Asn Ile Thr Ile Leu Val Val Val Ala Thr Glu Pro Val 55 160 Leu His Lys Pro Val Tyr Leu Phe Leu Cys Met Leu Ser Thr Ile Asp 161 65 7.0 164 Leu Ala Ala Ser Val Ser Thr Val Pro Lys Leu Leu Ala Ile Phe Trp 85 90 168 Cys Gly Ala Gly His Ile Ser Ala Ser Ala Cys Leu Ala His Met Phe 169 100 105 172 Phe Ile His Ala Phe Cys Met Met Glu Ser Thr Val Leu Leu Ala Met 173 115 120 176 Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Ala Thr 135 180 Ile Leu Thr Asp Thr Ile Ile Ala His Ile Gly Val Ala Ala Val Val 150 155 184 Arg Gly Ser Leu Leu Met Leu Pro Cys Pro Phe Phe Ile Gly Arg Leu 165 170 188 Asn Phe Cys Gln Ser His Val Ile Leu His Thr Tyr Cys Glu His Met 180 185 192 Ala Val Val Lys Leu Ala Cys Gly Asp Thr Arg Pro Asn Arg Val Tyr 195 200 196 Gly Leu Thr Ala Ala Leu Leu Val Ile Gly Val Asp Leu Phe Cys Ile 215 200 Gly Leu Ser Tyr Ala Leu Ile Ala Gln Ala Val Leu Arg Leu Ser Ser 201 225 230 235 204 His Glu Ala Arg Ser Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys 245 208 Val Ile Leu Ile Ser Tyr Thr Pro Ala Leu Phe Ser Phe Phe Thr His 260 265 212 Arg Phe Gly His His Val Pro Val His Ile His Ile Leu Leu Ala Asn 275 280 216 Val Tyr Leu Leu Pro Pro Ala Leu Asn Pro Val Val Tyr Gly Val 295 300 220 Lys Thr Lys Gln Ile Arg Lys Arg Val Val Arg Val Phe Gln Ser Gly 310 224 Gln Gly Met Gly Ile Lys Ala Ser Glu

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228 <210> SEQ ID NO: 3
229 <211> LENGTH: 320
230 <212> TYPE: PRT
231 <213> ORGANISM: Rattus norvegicus
233 <400> SEQUENCE: 3
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238 Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
239 20
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241 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
242 35
                           40
244 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
                          55
247 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
250 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
                  85
                                     90
253 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
254 100
                                 105
256 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
257 115 120
259 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
                         135
262 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu
                      150
                                        155
265 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
                  165
                                    170
268 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
             180
                                185
271 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
272 195
                            200
274 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
275 210
                         215
277 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
                      230
                                        235
280 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
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                                     250
283 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
284 260
                                265
286 Val Leu Met Gly Asp Val Tyr Leu Leu Pro Pro Val Ile Asn Pro
    275
                             280
289 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
290 290
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292 Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
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295 <210> SEQ ID NO: 4
296 <211> LENGTH: 320
297 <212> TYPE: PRT
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Input Set : A:\PTO.VSK.txt

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 305 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
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 308 Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
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 311 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
                            55
314 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
                        70
317 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
                    85
                                        90
320 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
               100
                                    105
323 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
           115
                                120
326 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
                            135
                                                140
329 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu
330 145
                        150
                                            155
332 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
                    165
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335 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
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338 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
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341 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
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344 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
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                                            235
347 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
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350 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
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                                    265
353 Val Val Met Gly Asp Ile Tyr Leu Leu Pro Pro Val Ile Asn Pro
           275
                                280
356 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
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359 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
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362 <210> SEQ ID NO: 5
363 <211> LENGTH: 318
364 <212> TYPE: PRT
365 <213> ORGANISM: homo sapiens
367 <400> SEQUENCE: 5
369 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe
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VERIFICATION SUMMARY

DATE: 03/20/2002 PATENT APPLICATION: US/10/081,775 TIME: 11:25:59

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 $\mbox{L:} 10 \mbox{ M:} 270 \mbox{ C: Current Application Number differs, Replaced Current Application NoL:} 10 \mbox{ M:} 271 \mbox{ C: Current Filing Date differs, Replaced Current Filing Date}$